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Patentanmeldung Nr. Patent application No. Demande de brevet n°

03007993.3

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.

R C van Dijk

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(Falls die Bezeichnung der Erfindung nicht angegeben ist, siehe Beschreibung.
If no title is shown please refer to the description.
Si aucun titre n'est indiqué se referer à la description.)

PDE4D in atherosclerosis or restenosis

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Case 21729

PDE4D in atherosclerosis or restenosis

Background:

The PDE4D phosphodiesterases exist in mammals in the form of isoenzymes (which represent different molecular forms of the same enzyme polypeptide). The PDE4D isoenzymes specifically degrade cAMP and are a common target for such pharmacological agents as antidepressants (for example, rolipram). Several splice forms of PDE4D are known. Among them are the long isoforms, of which 6 are known, namely PDE4D3, PDE4D4, PDE4D5, PDE4D6, PDE4D7 and PDE4D8. All of these have in common the LR1 and UCR1 sites and the domains located at the C-terminus of these sites, but they have different N-terminal domains. Isoform PDE4D5 was disclosed by Bolger et al., Characterization of five different proteins produced by alternatively spliced mRNAs from the human cAMP-specific phosphodiesterase PDE4D gene, Biochem. J.(1997), 328, 539-548. Isoform PDE4D7 was recently disclosed in WO02/074992. The PDE4D gene locus has been linked to stroke (WO02/074992). However, there has been no indication so far for an involvement of PDE4D in atherosclerosis or restenosis.

In the present invention PDE4D, more preferably PDE4D5 or PDE4D7, was identified as a novel target for the identification of compounds that can be used for the treatment of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease (PAOD), or for the treatment of restenosis.

HR/07.04.2003

Description

In the present invention, PDE4D was identified as a novel target for identifying coumpounds for therapy of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease (PAOD), or of restenosis. In a preferred embodiment, the novel target is PDE4D5 (Seq ID No. 4 and the homolog from other species) or PDE4D7 (Seq ID No. 1 to 3). In a most preferred embodiment, the novel target is PDE4D7. As shown in Figures 1 and 4, PDE4D5 and especially PDE4D7 are up-regulated in the media and intima of balloon-injured rat carotid arteries.

Thus, the present invention provides a novel use of the PDE4D, preferably of PDE4D5 or PDE4D7, for identifying a compound which inhibits atherosclerosis, preferably Peripheral Arterial Occlusive Disease (PAOD), or restenosis. Most preferably, PDE4D7 is used.

The present invention also provides a novel process for identifying and obtaining a compound for therapy of atherosclerosis, said process comprising measuring the activation or inhibition of the phosphodiesterase activity of PDE4D, preferably of PDE4D5 or PDE4D7, and a compound identified by said process. Most preferably, said compound is an inhibitor of PDE4D, preferably of PDE4D5 or PDE4D7. Most preferably, said compound is an inhibitor of PDE4D7. Procedures to measure phosphodiesterase activity are well known in the art. One non-limiting example for such an assay is described in the examples. The identification of compounds for therapy of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease, or of restenosis may also involve administration of compounds suspected to inhibit PDE4D, more preferably PDE4D5 or PDE4D7, most preferably PDE4D7, to an animal in which atherosclerosis, preferably Peripheral Arterial Occlusive Disease, or restenosis is induced, such as in the rat balloon-injury model, or, as another non-limiting example, in ApoE knockout mice which are fed a Western Type diet or a normal Chow diet as a control (eg described by Nakashima et al., ApoE-deficient

mice develop lesions of all phases of atherosclerosis throughout the arterial tree, Arterioscler. Thromb. (1994) Jan;14(1):133-40). Preferably, said animal is a non-human animal. Thus, the present invention also provides a process for identifying and obtaining a compound for therapy of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease, or restenosis, said process comprising administering a compound suspected to be an activator or inhibitor of PDE4D, preferably of PDE4D5 or PDE4D7, to an animal in which atherosclerosis, preferably Peripheral Arterial Occlusive Disease, or restenosis is induced, and measuring the extent of atherosclerosis, preferably of Peripheral Occlusive Disease, or restenosis as compared to placebo or carrier-treated animals.

A process for identifying activators or inhibitors for PDE4D may comprise using a core PDE4D construct (Seq ID No. 5) which is a PDE4D with an amino acid sequence common to all PDE4D long form isoforms. Figure 5 shows an inhibition of core PDE4D activity by Rolipram.

As used herein, the term „activator or inhibitor of PDE4D" refers to compounds that activate or inhibit PDE4D cellular function, either by acting directly on the phosphodiesterase of PDE4D, or by modulating indirectly the function of PDE4D, eg. by altering its subcellular targeting.

Further to this, the present invention pertains to a pharmaceutical composition comprising an activator or inhibitor of the phosphodiesterase activity of PDE4D, preferably of PDE4D5 or PDE4D7, identified by the process herein before described, and a pharmaceutically acceptable carrier. Most preferably, said pharmaceutical composition comprises an inhibitor of PDE4D.

The phrase "pharmaceutically acceptable" is employed herein to refer to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues of human beings and animals without excessive toxicity, irritation, allergic response, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

As used herein, "pharmaceutically acceptable salts" refer to derivatives of the identified agents wherein the parent agent is modified by making acid or base salts thereof. Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or

organic acid salts of basic residues such as amines; alkali or organic salts of acidic residues such as carboxylic acids; and the like. The pharmaceutically acceptable salts include the conventional non-toxic salts or the quaternary ammonium salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. For example, such conventional non-toxic salts include those derived from inorganic acids such as hydrochloric, hydrobromic, sulfuric, sulfamic, phosphoric, nitric and the like; and the salts prepared from organic acids such as acetic, propionic, succinic, glycolic, stearic, lactic, malic, tartaric, citric, ascorbic, pamoic, maleic, hydroxymaleic, phenylacetic, glutamic, benzoic, salicylic, sulfanilic, 2-acetoxybenzoic, fumaric, benzenesulfonic, toluenesulfonic, methanesulfonic, ethane disulfonic, oxalic, isethionic, and the like.

The pharmaceutically acceptable salts of the present invention can be synthesized from the parent agent which contains a basic or acidic moiety by conventional chemical methods. Generally, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in water or in an organic solvent, or in a mixture of the two; generally, nonaqueous media like ether, ethyl acetate, ethanol, isopropanol, or acetonitrile are preferred. Lists of suitable salts are found in Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, PA, 1985, p. 1418, the disclosure of which is hereby incorporated by reference.

The agents identified by the method of the invention may be modified to achieve (i) modified site of action, spectrum of activity, and/or (ii) improved potency, and/or (iii) decreased toxicity (improved therapeutic index), and/or (iv) decreased side effects, and/or (v) modified onset of action, duration of effect, and/or (vi) modified kinetic parameters (resorption, distribution, metabolism and excretion), and/or (vii) modified physico-chemical parameters (solubility, hygroscopicity, color, taste, odor, stability, state), and/or (viii) improved general specificity, organ/tissue specificity, and/or (ix) optimized application form and route by (i) esterification of carboxyl groups, or (ii) esterification of hydroxyl groups with carbon acids, or (iii) esterification of hydroxyl groups to, e.g. phosphates, pyrophosphates or sulfates or hemi succinates, or (iv) formation of pharmaceutically acceptable salts, or (v) formation of pharmaceutically acceptable complexes, or (vi) synthesis of pharmacologically active polymers, or (vii) introduction of hydrophilic moieties, or (viii) introduction/exchange of substituents on aromates or side chains, change of substituent pattern, or (ix) modification by introduction of isosteric or bioisosteric moieties, or (x) synthesis of homologous compounds, or (xi) introduction of branched side chains, or (xii) conversion of alkyl substituents to cyclic analogues, or (xiii) derivatisation of hydroxyl group to ketales, acetales, or (xiv) N-acetylation to amides, phenylcarbamates, or (xv) synthesis of Mannich bases, imines, or (xvi) transformation of ketones or aldehydes to Schiff's bases, oximes, acetales, ketales, enolesters, oxazolidines,

thiozolidines or combinations thereof; and (b) formulating the product of said modification with a pharmaceutically acceptable carrier or a carrier/diluent acceptable for fragrance or flavor compositions or products.

Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as flavoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

In one embodiment, a method of the present invention involves the administration of a therapeutically effective amount of an antisense oligonucleotide having a sequence capable of binding specifically with any sequences of genomic DNA or an mRNA molecule which encodes PDE4D, or preferably PDE4D5 or PDE4D7, so as to prevent transcription or translation of PDE4D mRNA, preferably PDE4D5 or PDE4D7 mRNA, most preferably PDE4D7 mRNA. By "antisense" is meant a composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Once introduced into a cell, the complementary nucleotides combine with endogenous sequences produced by the cell to form duplexes and to block either transcription or translation. See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama et al. (1997) Pharmacol. Res. 36:171-178; Crooke, S.T. (1997) Adv. Pharmacol. 40:1-49; and Lavrosky et al. (1997) Biochem. Mol. Med. 62(1):11-22. Antisense sequences can be any nucleic acid material, including DNA, RNA, or any nucleic acid mimics or analogs. See, e.g., Rossi et al. (1991) Antisense Res. Dev. 1:285-288; Pardridge et al. (1995) Proc. Nat. Acad. Sci. 92:5592-5596; Nielsen and Haaima (1997) Chem. Soc. Rev. 96:73-78; and Lee et al. (1998) Biochemistry 37:900-1010. Delivery of antisense sequences can be accomplished in a variety of ways, such as through intracellular delivery using a recombinant vector.

Antisense oligonucleotides of about 15 to 25 nucleic acid bases are typically preferred as such are easily synthesized and are capable of producing the desired inhibitory effect. Molecular analogs of antisense oligonucleotides may also be used for this purpose and can have added advantages such as stability, distribution, or limited toxicity advantageous in a pharmaceutical product. In addition, chemically reactive groups, such as iron-linked ethylenediamine-tetraacetic acid (EDTA-Fe), can be attached to antisense

oligonucleotides, causing cleavage of the RNA at the site of hybridization. These and other uses of antisense methods to inhibit the *in vitro* translation of genes are well known in the art. See, e.g., Marcus-Sakura (1988) Anal. Biochem. 172:289.

Inhibition of PDE4D, preferably PDE4D5 or PDE4D7, most perferably PDE4D7 may also be achieved by using RNA interference. RNA interference may be obtained, as a non-limiting example, by the process disclosed in GB 2372995 for inhibiting the expression of a target gene in cells or tissue comprises infection of said cells or tissue with (a) viral particles containing single stranded ribonucleic acid (ss RNA) expressing a sense RNA strand and (b) viral particles containing single stranded ribonucleic acid (ss RNA) expressing an anti-sense RNA strand, wherein the sense and anti-sense RNA strands comprise homologous nucleotide sequences to a portion of said target gene.

Rat carotid arteriy ballon injury is a well accepted technology to study the proliferative events in arteries. It was originally used to help the analysis of the smooth muscle cell proliferative component of atherosclerosis, but recently was also used as a model of restenosis after angioplasty. The SMC response to injury is similar in femoral and carotid arteries. Since it is technically much easier and experimentally much more reproducible the model was applied to the carotid artery. By all means it is intended to serve as model of a hall mark of Peripheral Arterial Occlusive Disease PAOD which is atherosclerosis in femoral arteries. As shown in Table 1, the PDE4 inhibitor Rolipram inhibits neointima formation in this model.

Thus, the present invention also provides a method of treatment of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease, or of restenosis comprising administering an activator or inhibitor of PDE4D, preferably of PDE4D5 or PDE4D7 to a subject suffering of atherosclerosis, preferably Peripheral Arterial Occlusive Disease, or restenosis. In a most preferred embodiment, an inhibitor of PDE4D, preferably of PDE4D5 or PDE4D7, most preferably of PDE4D7 is administered. Thus, the present invention pertains to the use of an activator or inhibitor of PDE4D, preferably PDE4D5 or PDE4D7 for the preparation of a medicament for the treatment of atherosclerosis, restenosis or, preferably, Peripheral Arterial Occlusive Disease. In a most preferred embodiment, an inhibitor of PDE4D, preferably of PDE4D5 or PDE4D7, most preferably of PDE4D7, is used.

The present invention also provides the compounds, processes, uses and compositions substantially as hereinbefore described, especially with reference to the foregoing examples.

Brief description of the figures:

Figure 1:

On the left panel, the catheter injured carotid samples are shown on top. Clearly, a ca. 80 kDa protein is detected with the affinity-purified anti-PDE4D7 rabbit polyclonal antibody. PDE4D7 was neither detected in the non-injured right carotid (left panel, bottom) nor in the control carotids from untreated animals (right panel), indicating a strong induction of PDE4D7 expression as a consequence of balloon catheter injury.

Figure 2:

A: Cross-reactivity human and rat PDE4D5 N-terminus: human and rat PDE4D5 are 98.85% identical.

B: The comparisons between UCR1, UCR2 and the catalytic domains of the PDE4 subfamilies A, B, C and D show that the UCRs are about as well-conserved as the catalytic domain.

Figure 3:

Cross reactivity human-rat-mouse PDE4D7:

Q8CG05: mouse PDE4D7 (Seq ID No. 1); Q8CH04: rat PDE4D7 (Seq ID No. 2); Q8IVD2: human PDE4D7 (Seq ID No. 3)

human-rat: 96.8 %

rat-mouse: 98.8 %

Figure 4:

PDE4D5 and PDE4D7 expression in balloon-injured rat carotids

Lanes 1,2,3: Media and intima, balloon-injured, left carotid, 3 days post balloon inury

Lanes 4,5,6: Media, right carotis (uninjured, control), 3 days

Lane 7: media and intima, balloon-injured, left carotid, 14 d post injury

Lane 8: right carotid, non-injured, control, 14 days

Lanes 9,10: media and intima, balloon-injured, left carotid, 7 days post injury

Lanes 11,12: right carotid, non-injured, 7 days

Figure 5:

Rolipram inhibition. Phosphodiesterase activity of the PDE4D core construct (DC) can be inhibited by Rolipram. The IC50 of DC phosphodiesterase activity by Rolipram inhibition was 0.34+/- 0.06 mM.

Examples

PDE4D5 and PDE4D7 expression in injured rat carotid arteries

Animal surgery

Male (300 - 400g) Wistar Kyoto Rats (RoRo) were obtained from BRL CH-Füllinsdorf. The animals were anaesthetized with 5mg/kg Xylazine (Rhompun, Bayer, FRG) and 50mg/kg Ketamin (Ketasol 100, Graeub, CH) i.p. The left carotid was exposed at the bifurcation and a 2F embolectomy catheter (Edwards laboratories, USA) was inserted.

The inflated balloon was pulled through the common carotid artery three times. After permanent ligation of the external carotid artery the wound was closed and the animals kept in pairs with commercial chow and water ad libidum.

Tissue harvest

6 weeks post injury the animals were reanesthesized and killed with an i.v. overdose of anesthetics. After opening the body cavity, rats are perfused with cold PBS via a catheter placed in the aortic arch to flush out the blood, and the carotid arteries harvested. The adventitial issues were removed from the arteries with watchmaker forceps. The carotids were opened longitudinally and any remaining endothelium was removed by sliding movements of the forceps. The carotids consist now only of smooth muscle cell tissue. At this stage the carotids were shock frozen in liquid nitrogen, pooled and stored at –80 degrees Celsius.

Experimental groups

4 experimental groups were pooled:

1. 11 balloon injured carotids 6 weeks post ballooning
2. 11 contralateral uninjured carotid arteries
3. 12 left carotids of unmanipulated rats
4. 12 contralateral right carotids form unmanipulated rats

Antibodies

An anti-peptide antibody was generated based on the specific sequence in human PDE4D7 (H_2N-CADLKSESENIQRPTS-$CONH_2$). This antibody was purified using the column-bound synthetic peptide for affinity chromatography. The specificity of this antibody was tested by Western blotting using recombinant preparations of human PDE 4D3, PDE4D5, PDE4D6, PDE4D7, PDE4D8 as samples. The antibody exclusively detected hPDE4D7 in these experiments. The ability of the antibody to cross-react with rat or

mouse is suggested by the high degree of conservation between human, rat or mouse PDE4D7, as shown in Figure 3.

An anti-PDE4D5 peptide antibody was prepared and characterized in a similar way based on the specific sequence H_2N -CEKSKTARKSVSPKLSP- $CONH_2$. Again, the ability to cross-react is suggested by the high degree of identity in the N-terminal portion of human and rat PDE4D5, as shown in Figure 2.

Preparation of samples for Two-Dimensional Electrophoresis

The frozen carotid arteries were powdered in a mortar with liquid nitrogen cooling. The homogenate was taken up in sample solution (7 M urea, 2 M thiourea, 50 mM Tris, 2% (w/v) CHAPS (2-[(3-Cholamidopropyl)dimethyl-ammonio]1-propane sulfonate, Roche Diagnostics, Mannheim, Germany), 0.4% (w/v), Dithioerythritol, 0.5% (v/v) ampholytes (Resolytes 3.5 – 10, BDH, Poole, England)) and left at room temperature for 15 min. The homogenate was centrifuged at 100,000 x g for 1 h at 4°C and the supernatant was collected. The protein concentration was estimated using the BioRad protein assay.

Two-Dimensional Polyacrylamide Gel Electrophoresis

Immobilized pH gradient strips (11cm, pH 4 – 7, Amersham Biosciences, Little Chalfont, England) were re-swollen in 7 M urea, 2 M thiourea, CHAPS, 0.4% (w/v), Dithioerythritol, 0.5% (v/v) ampholytes for 6 h, and placed into a Protean IEF cell cup loading tray (BioRad, Hercules, CA). Equal protein amounts (0.5 mg) of the samples were loaded into the cups and isoelectric focusing was performed using the following protocol: 250 V, 2h; gradual increase to 2500 V over 8 h; 2500 V for 8 h. The strips were equilibrated by two consecutive incubations in 6 M urea, 50 mM Tris-HCl, pH 7.5, 30% (v/v) glycerol, 2% (w/v) SDS, 30 mM Dithioerythritol, and in 6 M urea, 50 mM Tris-HCl, pH 7.5, 30% (v/v) glycerol, 2% (w/v) SDS, 136 mM Thioacetamide for 15 min each. The equilibrated strips were placed into the IEF well of a Criterion 4-15% gels. SDS-polyacrylamide electrophoresis and blotting to nitrocellulose membranes (BioRad) was performed according to the gel manufacturer's recommendations. A molecular weight marker (Magic Marker, Invitrogen) was included for molecular weight estimation.

Western Blotting

The blots were blocked with 5% non-fat dry milk in TBS with shaking overnight at 4°C. After washing, 100 ng/ml of the affinity-purified anti-PDE4D7 antibody in TBS + 0.1% (v/v) Tween 20 was added and the blots were incubated with shaking for 90 min at room temperature. The blots were washed and peroxidase-conjugated anti-rabbit antibody was added (dilution 1/50000, BioRad) and incubated with the blots for another 90 min. After washing, the blots were developed with Super Signal West Femto substrate (PIERCE, Rockford, IL) and exposed to film for 5 – 10 min.

Inhibition of neointima formation in balloon catheter injured rat carotid arteries by the PDE4 inhibitor rolipram

Drug application

Rolipram at appropriate concentration was prepared in PEG400 (25mg or 2.5mg/ml) and loaded into osmotic minipumps (2002 Alzet) to deliver a constant dose of 0.8 or 8mg/kg/d respectively per rat. The minipump was placed sc. in the neck position of the rat under anesthesia during surgery for the balloon catheter injury. The minipump was connected to the jugular vein via a sylastic catheter to ensure constant i.v. infusion over the entire experimental period of 14d.

Plasmalevels were determined at the end of the experiment using LCMSMS.

Results following balloon catheter injury (see under animal surgery above):

As shown in Table 1, rolipram inhibited neointima formation in balloon catheter injured rat carotid arteries significantly at 0.8 and 8mg/kg/day iv. To confirm the results, the higher dose was repeated in an independent experiment with a new set of rats (exp 2). At the end of the experiment still 20% of the original volume is present in the pumps due to the slower pumprate of a PEG 400 solution rather than water. Thus, the plasma levels determined at the end of the experiment reflect steady state exposure. It is interesting to note that plasma levels are well within the expected range of Ki of Rolipram for PDE4 enzymes

Experiment (number)	Rolipram dose (mg/kg/d)	Inhibition of neointima (% from placebo)	plasma level (nM)	p	n
2002-33	8	48	570±70	>0.05	10
2002-33	0.8	33	70±24	>0.05	10
2003-2	8	37	420±150	>0.05	9

<u>Table1</u> shows the summary of the efficacy data of rolipram mediated inhibition of neointima formation as measured by histomorphometry on plastic embedded cross sections (2 per carotid).

Expression of recombinant PDE4D5 and PDE4D7 isoforms

<u>Cloning of the PDE4D isoforms 5 and 7 and the core construct</u>

Core construct:

A cDNA encoding the core fragment that is common for all the PDE4D isoforms 3-8 starting with the amino acid sequence FDV carboxyterminal to the LF1 splice site was generated by PCR using a 5' oligonucleotide with a HindIII cloning site (gatgaattcaagctttttgatgtggacaatggcaca) introducing two additional amino acid (K and L) in front of the FDV sequence. At the 3' end a set of primers was used that either generated the native sequence (gtgatatctcattatcacgtgtcaggagaacgatcatctatgaca) or added a sequence encoding 6xHis residues (gtgatatctcattatcaa tgggatggtgatggtgcgtgtcaggagaacgatcatctatgac) to enable rapid purification of the recombinant proteins. The cDNA encoding the core construct was cloned as a EcoRI-EcoRV fragment into the expression vector pENTR™1a (GIBCO/BRL)

Isoforms (except core construct):

The DNA fragments encoding the isoform specific N-termini were generated by using synthetic oligonucleotides with terminal restriction enzyme sites for EcoRI and HindIII incorporated for directional cloning. These isoform specific DNA fragments were fused to the core construct sequence via the HindIII site introducing two additional amino acid residues (K and L). The integrity of the clones was confirmed by DNA sequencing prior to expression.

Expression of the PDE4D isoforms and the core construct in insect cells

The cDNAs were cloned into the pFASTBAC1 vector (Life Technologies. Inc) for expression in insect cells and the products were confirmed by sequencing. After recombination into the baculovirus genome the purified viral DNAs were transformed into the insect cells. Sf9 cells were cultured at 27^{0}C in TC100 medium (BioWhittaker) with 5% (v/v) fetal calf serum. Virus stocks were generated with a titer of 1.5x 10^9 pfu/ml. For large scale production of the isoforms 1-24 L fermentations of Sf9 cells were infected with a MOI of 1.

In one example, the 6xHis tagged PDE4D polypeptides DC, D5 and D7 were produced in Sf9 cells in 1L spinner flasks using SF1 medium in the absence of serum. Infected cells were harvested 3 days after infection with the recombinant baculoviruses.

In another example, the PDE4D core construct DC was produced in a 24 L Airlifter Fermenter with 15 L medium (SF1 with 0% serum), 0.15 L lipids and 9 L Sf9 cells. During the entire fermentation procedure the cells were cultured at pH 6.2, 27.0+/- 0.2°C and a pO_2 of 30.0+/- 0.5 %. Cells were grown for 3 days. The cell number at infection was 2.3x10^6 cells/ml. Cells were infected with 450 ml recombinant baculovirus. Cells were harvested at 68h post infection and the cell pellet as well as the cconcentrated supernatant stored at -80°C until further processing.

Purification of 6xHis tagged PDE4D isoforms

Sf9 cells from 1 liter culture broth, overexpressing the respective isoform, were resuspended on ice in 50 ml 50 mM HEPES pH 7.8, 300 mM NaCl 10 mM imidazole, 1 mM DTT, supplemented with protease inhibitors (one protease inhibitor cocktail tablet "complete, EDTA-free"; Roche). Opening of cells was performed by use of a 50 ml Dounce homogenizator and the homogeneous mixture was centrifuged for 1 hour at 70'000 g and 4°C (Kontron TFT 45.94 rotor at 30'000 rpm). The supernate was filtrated through a filter with a pore size of 1.2 µM (Minisart; Sartorius, Germany) and then applied to a 6 ml Ni-NTA agarose column at 2 ml/min. After equilibration with 50 mM HEPES pH 7.8, 300 mM NaCl, 10 mM imidazole, protein was eluted with a linear 30 ml gradient from 10 to 230 mM imidazole in the same buffer. Fractions containing the PDE4D isoform as analyzed by Coomassie stained SDS-PAGE were pooled and stored frozen at –80°C. Fresh Ni-NTA agarose material was used for every different PDE4D isoform preparation in order to prevent cross contamination of isoforms.

Specific activities of 6xHis tagged PDE4D isoforms

Relative concentrations of Ni-NTA agarose purified isoform preparations were estimated by SDS-PAGE. Equal volume amounts of isoform preparations were applied to a gradient gel (4-12% NuPage; Invitrogen). After electrophoresis the Coomassie stained polyacrylamide gel was imaged by a video imaging system. Optical densities of PDE4D bands were integrated using a Macintosh computer and the public domain software "NIH Image", version 1.61 (developed at the U.S. National Institutes of Health and available on the Internet at http://rsb.info.nih.gov/nih-image/). The integrated arbitrary units per PDE4D band as returned by the software reflect the relative PDE4D concentrations within the original pools. Identities of PDE4D and tubulin bands had been verified by independent SDS-PAGE, excision of corresponding bands, trypsin cleavage and identification of tryptic peptides by MALDI-MS.

Activities of equal volume amounts of 10^6-fold diluted purified isoforms were determined by use of a commercial radioactive phosphodiesterase assay (cAMP-dependent phosphodiesterase [^{3}H] assay; Amersham Pharmacia Biotech), following the instructions of the manufacturer. The obtained arbitrary activity units reflect the relative PDE4D activities within the original pools.

Relative specific activities of PDE4D isoforms were calculated by dividing relative activity values by relative concentration values.

Qualitative investigation of aggregation by size exclusion chromatography (SEC)

50 µl of Ni-NTA agarose purified isoform preparation was injected into a Superose 12 size exclusion column (type PC3.2/30; Amersham Pharmacia Biotech), equilibrated with 50 mM TrisHCl pH 7.7, 100 mM NaCl, 0.5 mM MgCl2 at a flow rate of 0.1 ml/min at 4°C. Chromatograms were recorded at 278 nm. Starting from the elution volume, the column eluate was collected as 50 µl fractions.

Activity assay and inhibition of phosphodiesterase activity

An IMAP FP-Assay was used for the determination of phosphodiesterase activity. The phosphodiesterase activity of the core contruct and PDE4D3, 5 or 7 was measured using the HEFP Phosphodiesterase Assay Kit (Molecular Devices). 2 µl of PDE4D5 or 7 or PDE4D core construct, 2 µl of cAMP (to a final concentration of 40 nM) and 1 µl of test substance or carrier were incubated for 45 min on a shaker. 12 µl of Binding Solution provided by the kit (with beads diluted 1:320) were added, and the reaction mixture incubated on a shaker for 2 hours. Fluorescence polarisation of the samples was measured in a Packard BioScience Fusion a-FP HT using as an emission filter a Polarizer 535, and as an excitation filter, Fluorescein 485/20. Inhibition of the phosphodiesterase activity of the PDE4D core construct was determined using Rolipram as inhibitor, and using PDE4D core construct at 30 ng/ml.

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> PDE4D in atherosclerosis or restenosis

<130> Case 21729

<160> 4

<170> PatentIn version 3.1

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Ser Glu Asn Ile Pro Arg Pro Thr Ser Leu Pro Leu Lys Ile Leu Pro

65 70 75 80

Leu Ile Ala Val Thr Ser Ala Asp Ser Thr Gly Phe Asp Val Asp Asn
85 90 95

Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly
100 105 110

Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu
115 120 125

Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser
130 135 140

Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu
145 150 155 160

Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg
165 170 175

Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys
180 185 190

Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr
195 200 205

Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp
210 215 220

Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser
225 230 235 240

Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr
245 250 255

His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Tyr Ile
260 265 270

Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro
275 280 285

Thr Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser

290 295 300

Gly Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Cys Ile

305 310 315 320

Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu

325 330 335

Leu Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu

340 345 350

Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln

355 360 365

Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile

370 375 380

Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr

385 390 395 400

His Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu

405 410 415

Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu

420 425 430

Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val

435 440 445

Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr

450 455 460

Asn Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys

465 470 475 480

Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys

485 490 495

Gln Arg Gln Ser Leu Arg Lys Met Ala Ile Asp Ile Val Leu Ala Thr

500 505 510

Asp Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val

515 520 525

Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr

530 535 540

Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu

545 550 555 560

Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg

565 570 575

Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly

580 585 590

Met Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys

595 600 605

Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr

610 615 620

Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu

625 630 635 640

Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser

645 650 655

Pro Ala Pro Asp Asp Gln Glu Asp Gly Arg Gln Gly Gln Thr Glu Lys

660 665 670

Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu

675 680 685

Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser

690 695 700

Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp

705 710 715 720

Glu Gln Val Glu Glu Glu Ala Val Ala Glu Glu Glu Ser Gln Pro Gln

725 730 735

Thr Gly Val Ala Asp Asp Cys Cys Pro Asp Thr

740 745

<210> 2

<211> 747

<212> PRT

<213> Rattus norvegicus

<220>

<221> rat PDE4D7

<222> (1)..(747)

<223>

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1 5 10 15

Glu Glu Thr Leu His Ser Cys Asn Glu Glu Glu Asp Pro Phe Arg Gly

20 25 30

Met Glu Pro Tyr Leu Val Arg Arg Leu Ser Ser Arg Ser Ile Gln Leu

35 40 45

Pro Pro Leu Ala Phe Arg Gln Leu Glu Gln Ala Asp Leu Arg Ser Glu

50 55 60

Ser Glu Asn Ile Pro Arg Pro Thr Ser Leu Pro Leu Lys Ile Leu Pro

65 70 75 80

Leu Ile Ala Val Thr Ser Ala Asp Ser Ser Gly Phe Asp Val Asp Asn
85 90 95
Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly
100 105 110
Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu
115 120 125
Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser
130 135 140
Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu
145 150 155 160
Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg
165 170 175
Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys
180 185 190
Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr
195 200 205
Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp
210 215 220
Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser
225 230 235 240
Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr
245 250 255
His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Tyr Ile
260 265 270
Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro
275 280 285

Thr Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser

290 295 300

Gly Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Cys Ile

305 310 315 320

Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu

325 330 335

Leu Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu

340 345 350

Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln

355 360 365

Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile

370 375 380

Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr

385 390 395 400

His Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu

405 410 415

Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu

420 425 430

Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val

435 440 445

Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr

450 455 460

Asn Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys

465 470 475 480

Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys

485 490 495

Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr

500 505 510

Asp Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val

515 520 525

Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr

530 535 540

Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu

545 550 555 560

Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg

565 570 575

Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly

580 585 590

Met Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys

595 600 605

Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr

610 615 620

Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu

625 630 635 640

Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser

645 650 655

Pro Ala Pro Asp Asp Gln Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys

660 665 670

Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Cys Glu Ser Asp Thr Glu

675 680 685

Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser

690 695 700

Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp

705 710 715 720

Glu Gln Val Glu Glu Glu Ala Val Ala Glu Glu Glu Ser Gln Pro Glu

725 730 735

Thr Cys Val Pro Asp Asp Cys Cys Pro Asp Thr

740 745

<210> 3

<211> 748

<212> PRT

<213> Homo sapiens

<220>

<221> human PDE4D7

<222> (1)..(748)

<223>

<400> 3

Met Lys Arg Asn Thr Cys Asp Leu Leu Ser Arg Ser Lys Ser Ala Ser

1 5 10 15

Glu Glu Thr Leu His Ser Ser Asn Glu Glu Glu Asp Pro Phe Arg Gly

20 25 30

Met Glu Pro Tyr Leu Val Arg Arg Leu Ser Cys Arg Asn Ile Gln Leu

35 40 45

Pro Pro Leu Ala Phe Arg Gln Leu Glu Gln Ala Asp Leu Lys Ser Glu

50 55 60

Ser Glu Asn Ile Gln Arg Pro Thr Ser Leu Pro Leu Lys Ile Leu Pro

65 70 75 80

Leu Ile Ala Ile Thr Ser Ala Glu Ser Ser Gly Phe Asp Val Asp Asn

85 90 95

Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly

100 105 110

Ser Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu

115 120 125

Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser

130 135 140

Met Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu

145 150 155 160

Ile Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg

165 170 175

Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys

180 185 190

Arg Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr

195 200 205

Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp

210 215 220

Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser

225 230 235 240

Glu Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr

245 250 255

His Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile

260 265 270

Ser Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro

275 280 285

Thr Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser

290 295 300

Gly Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile

305 310 315 320

Pro Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu

325 330 335

Leu Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu

340 345 350

Leu Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln

355 360 365

Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile

370 375 380

Thr Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr

385 390 395 400

His Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu

405 410 415

Leu Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu

420 425 430

Ala Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val

435 440 445

Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr

450 455 460

Asn Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys

465 470 475 480

Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys

485 490 495

Gln Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr

500 505 510

Asp Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val

515 520 525

Glu Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr

530 535 540

Ser Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu

545 550 555 560

Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg

565 570 575

Ile Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly

580 585 590

Met Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys

595 600 605

Ser Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr

610 615 620

Trp Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu

625 630 635 640

Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser

645 650 655

Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys

660 665 670

Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu

675 680 685

Lys Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser

690 695 700

Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp

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Glu Gln Val Glu Glu Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro

725 730 735

Glu Ala Cys Val Ile Asp Asp Arg Ser Pro Asp Thr

740 745

<210> 4

<211> 747

<212> PRT

<213> Homo sapiens

<220>

<221> human PDE4D5

<222> (1)..(747)

<223>

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1 5 10 15

Asn Pro His Cys Pro Asn Pro Trp Leu Asn Glu Asp Leu Val Lys Ser

20 25 30

Leu Arg Glu Asn Leu Leu Gln His Glu Lys Ser Lys Thr Ala Arg Lys

35 40 45

Ser Val Ser Pro Lys Leu Ser Pro Val Ile Ser Pro Arg Asn Ser Pro

50 55 60

Arg Leu Leu Arg Arg Met Leu Leu Ser Ser Asn Ile Pro Lys Gln Arg

65 70 75 80

Arg Phe Thr Val Ala His Thr Cys Lys Leu Phe Asp Val Asp Asn Gly

85 90 95

Thr Ser Ala Gly Arg Ser Pro Leu Asp Pro Met Thr Ser Pro Gly Ser

100 105 110

Gly Leu Ile Leu Gln Ala Asn Phe Val His Ser Gln Arg Arg Glu Ser

115 120 125

Phe Leu Tyr Arg Ser Asp Ser Asp Tyr Asp Leu Ser Pro Lys Ser Met

130 135 140

Ser Arg Asn Ser Ser Ile Ala Ser Asp Ile His Gly Asp Asp Leu Ile

145 150 155 160

Val Thr Pro Phe Ala Gln Val Leu Ala Ser Leu Arg Thr Val Arg Asn

165 170 175

Asn Phe Ala Ala Leu Thr Asn Leu Gln Asp Arg Ala Pro Ser Lys Arg

180 185 190

Ser Pro Met Cys Asn Gln Pro Ser Ile Asn Lys Ala Thr Ile Thr Glu

195 200 205

Glu Ala Tyr Gln Lys Leu Ala Ser Glu Thr Leu Glu Glu Leu Asp Trp

210 215 220

Cys Leu Asp Gln Leu Glu Thr Leu Gln Thr Arg His Ser Val Ser Glu

225 230 235 240

Met Ala Ser Asn Lys Phe Lys Arg Met Leu Asn Arg Glu Leu Thr His

245 250 255

Leu Ser Glu Met Ser Arg Ser Gly Asn Gln Val Ser Glu Phe Ile Ser

260 265 270

Asn Thr Phe Leu Asp Lys Gln His Glu Val Glu Ile Pro Ser Pro Thr

275 280 285

Gln Lys Glu Lys Glu Lys Lys Lys Arg Pro Met Ser Gln Ile Ser Gly

290 295 300

Val Lys Lys Leu Met His Ser Ser Ser Leu Thr Asn Ser Ser Ile Pro

305 310 315 320

Arg Phe Gly Val Lys Thr Glu Gln Glu Asp Val Leu Ala Lys Glu Leu

325 330 335

Glu Asp Val Asn Lys Trp Gly Leu His Val Phe Arg Ile Ala Glu Leu

340 345 350

Ser Gly Asn Arg Pro Leu Thr Val Ile Met His Thr Ile Phe Gln Glu

355 360 365

Arg Asp Leu Leu Lys Thr Phe Lys Ile Pro Val Asp Thr Leu Ile Thr

370 375 380

Tyr Leu Met Thr Leu Glu Asp His Tyr His Ala Asp Val Ala Tyr His

385 390 395 400

Asn Asn Ile His Ala Ala Asp Val Val Gln Ser Thr His Val Leu Leu

405 410 415

Ser Thr Pro Ala Leu Glu Ala Val Phe Thr Asp Leu Glu Ile Leu Ala

420 425 430

Ala Ile Phe Ala Ser Ala Ile His Asp Val Asp His Pro Gly Val Ser

435 440 445

Asn Gln Phe Leu Ile Asn Thr Asn Ser Glu Leu Ala Leu Met Tyr Asn

450 455 460

Asp Ser Ser Val Leu Glu Asn His His Leu Ala Val Gly Phe Lys Leu

465 470 475 480

Leu Gln Glu Glu Asn Cys Asp Ile Phe Gln Asn Leu Thr Lys Lys Gln

485 490 495

Arg Gln Ser Leu Arg Lys Met Val Ile Asp Ile Val Leu Ala Thr Asp

500 505 510

Met Ser Lys His Met Asn Leu Leu Ala Asp Leu Lys Thr Met Val Glu

515 520 525

Thr Lys Lys Val Thr Ser Ser Gly Val Leu Leu Leu Asp Asn Tyr Ser

530 535 540

Asp Arg Ile Gln Val Leu Gln Asn Met Val His Cys Ala Asp Leu Ser

545 550 555 560

Asn Pro Thr Lys Pro Leu Gln Leu Tyr Arg Gln Trp Thr Asp Arg Ile

565 570 575

Met Glu Glu Phe Phe Arg Gln Gly Asp Arg Glu Arg Glu Arg Gly Met

580 585 590

Glu Ile Ser Pro Met Cys Asp Lys His Asn Ala Ser Val Glu Lys Ser

595 600 605

Gln Val Gly Phe Ile Asp Tyr Ile Val His Pro Leu Trp Glu Thr Trp

610 615 620

Ala Asp Leu Val His Pro Asp Ala Gln Asp Ile Leu Asp Thr Leu Glu

625 630 635 640

Asp Asn Arg Glu Trp Tyr Gln Ser Thr Ile Pro Gln Ser Pro Ser Pro

645 650 655

Ala Pro Asp Asp Pro Glu Glu Gly Arg Gln Gly Gln Thr Glu Lys Phe

660 665 670

Gln Phe Glu Leu Thr Leu Glu Glu Asp Gly Glu Ser Asp Thr Glu Lys

675 680 685

Asp Ser Gly Ser Gln Val Glu Glu Asp Thr Ser Cys Ser Asp Ser Lys

690 695 700

Thr Leu Cys Thr Gln Asp Ser Glu Ser Thr Glu Ile Pro Leu Asp Glu

705 710 715 720

Gln Val Glu Glu Glu Ala Val Gly Glu Glu Glu Glu Ser Gln Pro Glu

725 730 735

Ala Cys Val Ile Asp Asp Arg Ser Pro Asp Thr

740 745

<210> 5

<211> 664

<212> PRT

<213> Homo sapiens

<220>

<221> core PDE4D

<222> (1)..(664)

<223>

<400> 5

Met Phe Asp Val Asp Asn Gly Thr Ser Ala Gly Arg Ser Pro Leu Asp

1 5 10 15

Pro Met Thr Ser Pro Gly Ser Gly Leu Ile Leu Gln Ala Asn Phe Val

20 25 30

His Ser Gln Arg Arg Glu Ser Phe Leu Tyr Arg Ser Asp Ser Asp Tyr

35 40 45

Asp Leu Ser Pro Lys Ser Met Ser Arg Asn Ser Ser Ile Ala Ser Asp

50 55 60

Ile His Gly Asp Asp Leu Ile Val Thr Pro Phe Ala Gln Val Leu Ala

65 70 75 80

Ser Leu Arg Thr Val Arg Asn Asn Phe Ala Ala Leu Thr Asn Leu Gln

85 90 95

Asp Arg Ala Pro Ser Lys Arg Ser Pro Met Cys Asn Gln Pro Ser Ile

100 105 110

Asn Lys Ala Thr Ile Thr Glu Glu Ala Tyr Gln Lys Leu Ala Ser Glu

115 120 125

Thr Leu Glu Glu Leu Asp Trp Cys Leu Asp Gln Leu Glu Thr Leu Gln

130 135 140

Thr Arg His Ser Val Ser Glu Met Ala Ser Asn Lys Phe Lys Arg Met

145 150 155 160

Leu Asn Arg Glu Leu Thr His Leu Ser Glu Met Ser Arg Ser Gly Asn

165 170 175

Gln Val Ser Glu Phe Ile Ser Asn Thr Phe Leu Asp Lys Gln His Glu

180 185 190

Val Glu Ile Pro Ser Pro Thr Gln Lys Glu Lys Glu Lys Lys Lys Arg

195 200 205

Pro Met Ser Gln Ile Ser Gly Val Lys Lys Leu Met His Ser Ser Ser

210 215 220

Leu Thr Asn Ser Ser Ile Pro Arg Phe Gly Val Lys Thr Glu Gln Glu

225 230 235 240

Asp Val Leu Ala Lys Glu Leu Glu Asp Val Asn Lys Trp Gly Leu His

245 250 255

Val Phe Arg Ile Ala Glu Leu Ser Gly Asn Arg Pro Leu Thr Val Ile

260 265 270

Met His Thr Ile Phe Gln Glu Arg Asp Leu Leu Lys Thr Phe Lys Ile

275 280 285

Pro Val Asp Thr Leu Ile Thr Tyr Leu Met Thr Leu Glu Asp His Tyr

290 295 300

His Ala Asp Val Ala Tyr His Asn Asn Ile His Ala Ala Asp Val Val

305 310 315 320

Gln Ser Thr His Val Leu Leu Ser Thr Pro Ala Leu Glu Ala Val Phe

325 330 335

Thr Asp Leu Glu Ile Leu Ala Ala Ile Phe Ala Ser Ala Ile His Asp

340 345 350

Val Asp His Pro Gly Val Ser Asn Gln Phe Leu Ile Asn Thr Asn Ser

355 360 365

Glu Leu Ala Leu Met Tyr Asn Asp Ser Ser Val Leu Glu Asn His His

370 375 380

Leu Ala Val Gly Phe Lys Leu Leu Gln Glu Glu Asn Cys Asp Ile Phe

385 390 395 400

Gln Asn Leu Thr Lys Lys Gln Arg Gln Ser Leu Arg Lys Met Val Ile

405 410 415

Asp Ile Val Leu Ala Thr Asp Met Ser Lys His Met Asn Leu Leu Ala

420 425 430

Asp Leu Lys Thr Met Val Glu Thr Lys Lys Val Thr Ser Ser Gly Val

435 440 445

Leu Leu Leu Asp Asn Tyr Ser Asp Arg Ile Gln Val Leu Gln Asn Met

450 455 460

Val His Cys Ala Asp Leu Ser Asn Pro Thr Lys Pro Leu Gln Leu Tyr

465 470 475 480

Arg Gln Trp Thr Asp Arg Ile Met Glu Glu Phe Phe Arg Gln Gly Asp

485 490 495

Arg Glu Arg Glu Arg Gly Met Glu Ile Ser Pro Met Cys Asp Lys His

500 505 510

Asn Ala Ser Val Glu Lys Ser Gln Val Gly Phe Ile Asp Tyr Ile Val

515 520 525

His Pro Leu Trp Glu Thr Trp Ala Asp Leu Val His Pro Asp Ala Gln

530 535 540

Asp Ile Leu Asp Thr Leu Glu Asp Asn Arg Glu Trp Tyr Gln Ser Thr

545 550 555 560

Ile Pro Gln Ser Pro Ser Pro Ala Pro Asp Asp Pro Glu Glu Gly Arg

565 570 575

Gln Gly Gln Thr Glu Lys Phe Gln Phe Glu Leu Thr Leu Glu Glu Asp

580 585 590

Gly Glu Ser Asp Thr Glu Lys Asp Ser Gly Ser Gln Val Glu Glu Asp

595 600 605

Thr Ser Cys Ser Asp Ser Lys Thr Leu Cys Thr Gln Asp Ser Glu Ser

610 615 620

Thr Glu Ile Pro Leu Asp Glu Gln Val Glu Glu Glu Ala Val Gly Glu

625 630 635 640

Glu Glu Glu Ser Gln Pro Glu Ala Cys Val Ile Asp Asp Arg Ser Pro

645 650 655

Asp Thr His His His His His His

660

<210> 6

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> human PDE4D5 N-terminal domain

<222> (1)..(87)

<223>

<400> 6

Met Ala Gln Gln Thr Ser Pro Asp Thr Leu Thr Val Pro Glu Val Asp

1 5 10 15

Asn Pro His Cys Pro Asn Pro Trp Leu Asn Glu Asp Leu Val Lys Ser

20 25 30

Leu Arg Glu Asn Leu Leu Gln His Glu Lys Ser Lys Thr Ala Arg Lys

35 40 45

Ser Val Ser Pro Lys Leu Ser Pro Val Ile Ser Pro Arg Asn Ser Pro

50 55 60

Arg Leu Leu Arg Arg Met Leu Leu Ser Ser Asn Ile Pro Lys Gln Arg

65 70 75 80

Arg Phe Thr Val Ala His Thr

85

<210> 7

<211> 88

<212> PRT

<213> Rattus norvegicus

<220>

<221> rat PDE4D5 N-terminal domain

<222> (1)..(88)

<223>

<400> 7

Met Ala Gln Gln Thr Thr Ser Pro Asp Thr Leu Thr Val Pro Glu Val
1 5 10 15

Asp Asn Pro His Val Pro Asn Pro Trp Leu Asn Glu Asp Leu Val Lys
20 25 30

Ser Leu Arg Glu Asn Leu Leu Gln His Glu Lys Ser Lys Thr Ala Arg
35 40 45

Lys Ser Val Ser Pro Lys Leu Ser Pro Val Ile Ser Pro Arg Asn Ser
50 55 60

Pro Arg Leu Leu Arg Arg Met Leu Leu Ser Ser Asn Ile Pro Lys Gln
65 70 75 80

Arg Arg Phe Thr Val Ala His Thr
85

Claims

1. Use of PDE4D for identifying a compound which inhibits atherosclerosis or restenosis.

2. The use of claim 1 wherein the PDE4D is PDE4D5 or PDE4D7.

3. The use of claim 1 wherein the PDE4D is PDE4D7.

4. The use of any of claims 1 to 3, wherein said compound inhibits Peripheral Arterial Occlusive Disease.

5. A process for identifying and obtaining a compound for therapy of atherosclerosis or restenosis, said process comprising measuring the activation or inhibition of the phosphodiesterase activity of PDE4D.

6. The process of claim 5 wherein the PDE4D is PDE4D5 or PDE4D7.

7. The process of claim 6 wherein the PDE4D is PDE4D7.

8. The process of any one of claims 5 to 7, wherein a compound is obtained for the treatment of Peripheral Arterial Occlusive Disease.

9. A process for identifying and obtaining a compound for therapy of atherosclerosis, or restenosis, said process comprising administering a compound suspected to be an

activator or inhibitor of PDE4D to an animal in which atherosclerosis, restenosis or Peripheral Arterial Occlusive Disease is induced, and measuring the extent of atherosclerosis, restenosis or Peripheral Occlusive Disease as compared to control-treated animals.

10. The process of claim 9 wherein the PDE4D is PDE4D5 or PDE4D7.

11. The process of claim 10 wherein the PDE4D is PDE4D7.

12. The process of any one of claims 9 to 11, wherein the compound is for the therapy of Peripheral Arterial Occlusive Disease.

13. A compound identified by the process of any one of claims 5 to 12.

14. A pharmaceutical composition comprising an a compound of claim 13 and a pharmaceutically acceptable carrier.

15. Use of a compound of claim 13 for the preparation of a medicament for the treatment of atherosclerosis, restenosis or, preferably, Peripheral Arterial Occlusive Disease.

16. The compounds, processes, uses and composition substantially as hereinbefore described, especially with reference to the foregoing examples.

***

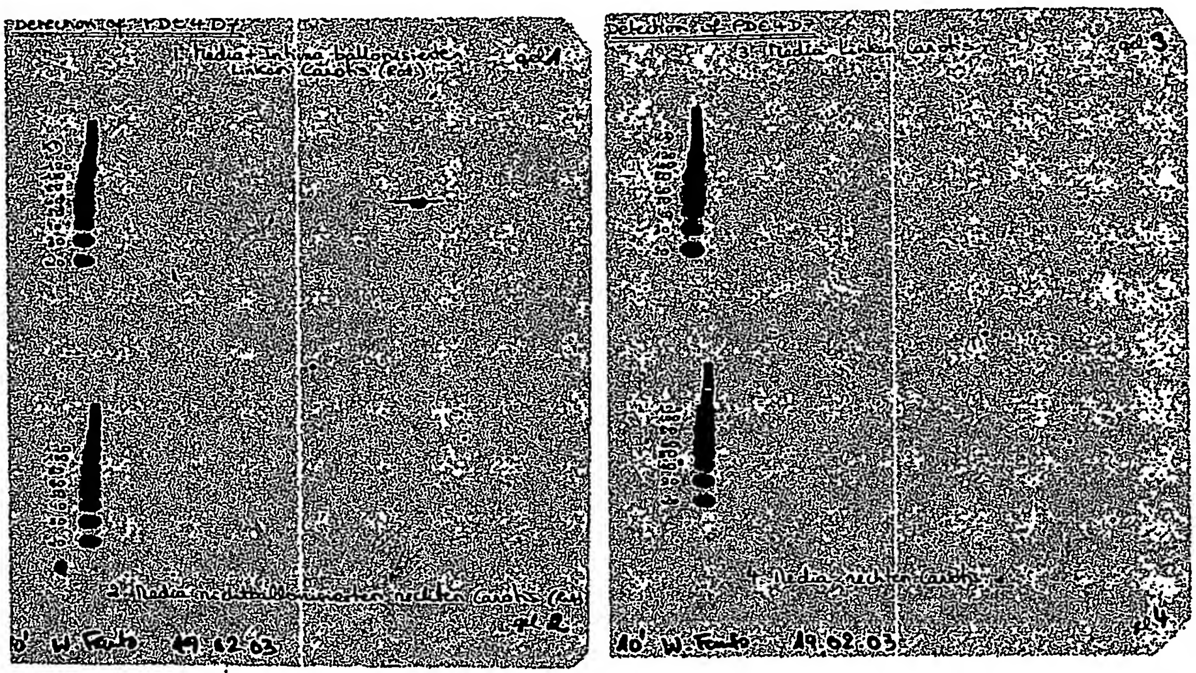
Abstract

The present invention provides the use of PDE4D, more preferably PDE4D5 or PDE4D7, as a novel target for the identification of compounds that can be used for the treatment of atherosclerosis, preferably of Peripheral Arterial Occlusive Disease (PAOD), or for the treatment of restenosis.

Figure 1

Media and intima
Balloon-injured, left carotis

Media, balloon-injured, left carotis



Media, non-injured, right carotis

Media, non-injured, right carotis

Figure 2

A. 4D5 N-terminus in man and rat

4D5 N-terminus: 98.85% identical

```
HUM.seq x RAT.seq          April 1, 2003 17:04  ..

       1 MAQQ.TSPDTLTVPEVDNPHCPNPWLNEDLVKSLRENLLQHEKSKTARKS 49
         |||| |||||||||||||||| |||||||||||||||||||||||||||||
       1 MAQQTTSPDTLTVPEVDNPHVPNPWLNEDLVKSLRENLLQHEKSKTARKS 50

      50 VSPKLSPVISPRNSPRLLRRMLLSSNIPKQRRFTVAHT 87
         ||||||||||||||||||||||||||||||||||||||
      51 VSPKLSPVISPRNSPRLLRRMLLSSNIPKQRRFTVAHT 88
```

B. Conserved sequence elements in the human PDE4 gene family

Comparisons:

UCR1

	A	B	C	D
A	+	83.1	79.3	79.7
B		+	79.3	86.4
C			+	86.2
D				+

UCR2

	A	B	C	D
A	+	88.6	78.2	84.8
B		+	79.5	89.9
C			+	83.3
D				+

Catalytic domain

	A	B	C	D
A	+	86.3	82.1	85.2
B		+	80.1	87.4
C			+	84.6
D				+

Figure 3/1

Q8CG05 - Mouse; Q8CG04 - Rat; Q8IVD2 - Human

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TR_ROD_Q8CG05    MERDTCDVLS RSKSASEETL HSCNEEEDPF RGMEPYLVRR LSSRSIQLPP
TR_ROD_Q8CG04    MERNTCDVLS RSKSASEETL HSCNDEEDPF RGMEPYLVRR LSSRSIQLPP
TR_HUM_Q8IVD2    MKRNTCDLLS RSKSASEETL HSSNEEEDPF RGMEPYLVRR LSCRNIQLPP

TR_ROD_Q8CG05    LAFRQLEQAD LRSESENIPR PTSLPLKILP LIAVTSADSS GFDVDNGTSA
TR_ROD_Q8CG04    LAFRQLEQTD LRSESENIPR PTSLPLKILP LIAVTSADST GFDVDNGTSA
TR_HUM_Q8IVD2    LAFRQLEQAD LKSESENIQR PTSLPLKILP LIAITSAESS GFDVDNGTSA

TR_ROD_Q8CG05    GRSPLDPMTS PGSGLILQAN FVHSQRRESF LYRSDSDYDL SPKSMSRNSS
TR_ROD_Q8CG04    GRSPLDPMTS PGSGLILQAN FVHSQRRESF LYRSDSDYDL SPKSMSRNSS
TR_HUM_Q8IVD2    GRSPLDPMTS PGSGLILQAN FVHSQRRESF LYRSDSDYDL SPKSMSRNSS

TR_ROD_Q8CG05    IASDIHGDDL IVTPFAQVLA SLRTVRNNFA ALTNLQDRAP SKRSPMCNQP
TR_ROD_Q8CG04    IASDIHGDDL IVTPFAQVLA SLRTVRNNFA ALTNLQDRAP SKRSPMCNQP
TR_HUM_Q8IVD2    IASDIHGDDL IVTPFAQVLA SLRTVRNNFA ALTNLQDRAP SKRSPMCNQP

TR_ROD_Q8CG05    SINKATITEE AYQKLASETL EELDWCLDQL ETLQTRHSVS EMASNKFKRM
TR_ROD_Q8CG04    SINKATITEE AYQKLASETL EELDWCLDQL ETLQTRHSVS EMASNKFKRM
TR_HUM_Q8IVD2    SINKATITEE AYQKLASETL EELDWCLDQL ETLQTRHSVS EMASNKFKRM

TR_ROD_Q8CG05    LNRELTHLSE MSRSGNQVSE YISNTFLDKQ HEVEIPSPTQ KEKEKKKRPM
TR_ROD_Q8CG04    LNRELTHLSE MSRSGNQVSE YISNTFLDKQ HEVEIPSPTQ KEKEKKKRPM
TR_HUM_Q8IVD2    LNRELTHLSE MSRSGNQVSE FISNTFLDKQ HEVEIPSPTQ KEKEKKKRPM

TR_ROD_Q8CG05    SQISGVKKLM HSSSLTNSCI PRFGVKTEQE DVLAKELEDV NKWGLHVFRI
TR_ROD_Q8CG04    SQISGVKKLM HSSSLTNSCI PRFGVKTEQE DVLAKELEDV NKWGLHVFRI
TR_HUM_Q8IVD2    SQISGVKKLM HSSSLTNSSI PRFGVKTEQE DVLAKELEDV NKWGLHVFRI

TR_ROD_Q8CG05    AELSGNRPLT VIMHTIFQER DLLKTFKIPV DTLITYLMTL EDHYHADVAY
TR_ROD_Q8CG04    AELSGNRPLT VIMHTIFQER DLLKTFKIPV DTLITYLMTL EDHYHADVAY
TR_HUM_Q8IVD2    AELSGNRPLT VIMHTIFQER DLLKTFKIPV DTLITYLMTL EDHYHADVAY

TR_ROD_Q8CG05    HNNIHAADVV QSTHVLLSTP ALEAVFTDLE ILAAIFASAI HDVDHPGVSN
TR_ROD_Q8CG04    HNNIHAADVV QSTHVLLSTP ALEAVFTDLE ILAAIFASAI HDVDHPGVSN
TR_HUM_Q8IVD2    HNNIHAADVV QSTHVLLSTP ALEAVFTDLE ILAAIFASAI HDVDHPGVSN
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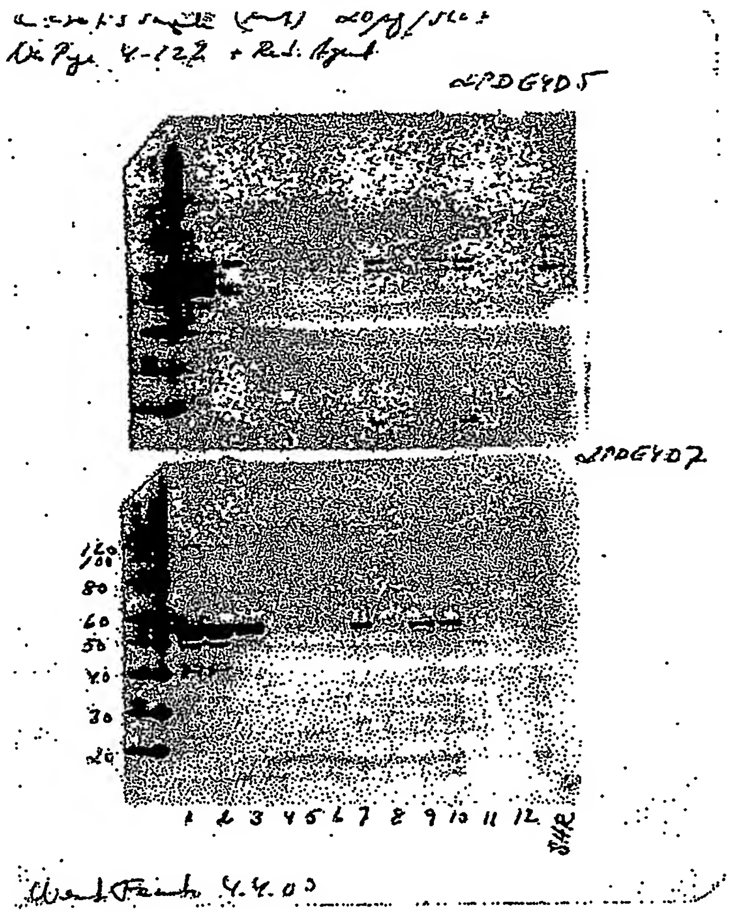
Figure 3/2

TR_ROD_Q8CG05	QFLINTNSEL	ALMYNDSSVL	ENHHLAVGFK	LLQEENCDIF	QNLTKKQRQS
TR_ROD_Q8CG04	QFLINTNSEL	ALMYNDSSVL	ENHHLAVGFK	LLQEENCDIF	QNLTKKQRQS
TR_HUM_Q8IVD2	QFLINTNSEL	ALMYNDSSVL	ENHHLAVGFK	LLQEENCDIF	QNLTKKQRQS
TR_ROD_Q8CG05	LRKMVIDIVL	ATDMSKHMNL	LADLKTMVET	KKVTSSGVLL	LDNYSDRIQV
TR_ROD_Q8CG04	LRKMAIDIVL	ATDMSKHMNL	LADLKTMVET	KKVTSSGVLL	LDNYSDRIQV
TR_HUM_Q8IVD2	LRKMVIDIVL	ATDMSKHMNL	LADLKTMVET	KKVTSSGVLL	LDNYSDRIQV
TR_ROD_Q8CG05	LQNMVHCADL	SNPTKPLQLY	RQWTDRIMEE	FFRQGDRERE	RGMEISPMCD
TR_ROD_Q8CG04	LQNMVHCADL	SNPTKPLQLY	RQWTDRIMEE	FFRQGDRERE	RGMEISPMCD
TR_HUM_Q8IVD2	LQNMVHCADL	SNPTKPLQLY	RQWTDRIMEE	FFRQGDRERE	RGMEISPMCD
TR_ROD_Q8CG05	KHNASVEKSQ	VGFIDYIVHP	LWETWADLVH	PDAQDILDTL	EDNREWYQST
TR_ROD_Q8CG04	KHNASVEKSQ	VGFIDYIVHP	LWETWADLVH	PDAQDILDTL	EDNREWYQST
TR_HUM_Q8IVD2	KHNASVEKSQ	VGFIDYIVHP	LWETWADLVH	PDAQDILDTL	EDNREWYQST
TR_ROD_Q8CG05	IPQSPSPAPD	DQEEGRQGQT	EKFQFELTLE	EDCESDTEKD	SGSQVEEDTS
TR_ROD_Q8CG04	IPQSPSPAPD	DQEDGRQGQT	EKFQFELTLE	EDGESDTEKD	SGSQVEEDTS
TR_HUM_Q8IVD2	IPQSPSPAPD	DPEEGRQGQT	EKFQFELTLE	EDGESDTEKD	SGSQVEEDTS
TR_ROD_Q8CG05	CSDSKTLCTQ	DSESTEIPLD	EQVEEEAVAE	EE.SQPETCV	PDDCCPDT
TR_ROD_Q8CG04	CSDSKTLCTQ	DSESTEIPLD	EQVEEEAVAE	EE.SQPQTGV	ADDCCPDT
TR_HUM_Q8IVD2	CSDSKTLCTQ	DSESTEIPLD	EQVEEEAVGE	EEESQPEACV	IDDRSPDT

Figure 4:

anti-PDE4D5



anti-PDE4D7

Figure 5

fluorescence polarization assay
30ng/ml PDE4D core construct IC_{50} Rolipram @40nMcAMP